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<!--StartFragment-->RESULT 1                                aAPPENDIX A: ALIGNMENT WITH SEQ ID NO 24
ADC00348
ID   ADC00348 standard; protein; 441 AA.
XX
AC   ADC00348;
XX
DT   15-JUN-2007 (revised)
DT   04-DEC-2003 (first entry)
XX
DE   Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 393.
XX
KW   enterohaemorrhagic; anti-bacterial; BOND_PC; hypothetical protein;
KW   hypothetical protein ECs1812 [Escherichia coli O157:H7];
KW   hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];
KW   unknown protein encoded by cryptic prophage CP-933P;
KW   hypothetical protein [Escherichia coli O157:H7 str. Sakai].
XX
OS   Escherichia coli; O157:H7.
XX
PN   JP2002355074-A.
XX
PD   10-DEC-2002.
XX
PF   24-JAN-2002; 2002JP-00015959.
XX
PR   24-JAN-2001; 2001JP-00112010.
XX
PA   (UYTS-) UNIV TSUKUBA.
XX
DR   WPI; 2003-451640/43.
DR   PC:NCBI; gi13259568.
XX
PT   Enterohemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT   and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX
PS   Claim 3; SEQ ID NO 393; 2067pp; Japanese.
XX
CC   The invention relates to a novel enterohaemorrhagic Escherichia coli
CC   O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC   has anti-bacterial activity. The polypeptide can be used in detection
CC   and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC   genome of Enterohaemorrhagic E coli O157:H7 was determined. The present
CC   sequence represents an E. coli O157:H7-specific polypeptide of the
CC   invention.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 441 AA;

Query Match          100.0%; Score 2341; DB 6; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.1e-197;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCGAGFVNNIPDDIQQHAPECGET 60
Db      1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCGAGFVNNIPDDIQQHAPECGET 60

Qy     61 TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY 120
Db     61 TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY 120

Qy    121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST 180
Db    121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST 180

Qy    181 GTSATTSTVTTEPKDIPWFGLTQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240

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      |||
Db      181  GTSATTSTVTTTEPKDIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240
Qy      241  TEEWVIRPGEADFKYGASPLQATLGLLEFGAHFKWDLNPNTRYAVLTNAAANALGALGGF 300
      |||
Db      241  TEEWVIRPGEADFKYGASPLQATLGLLEFGAHFKWDLNPNTRYAVLTNAAANALGALGGF 300
Qy      301  AVSRFASTDPMLSPHIGAMVGOAAGHAIQYNTPLGKPDITLWWAGATLGAADLNKAEFEV 360
      |||
Db      301  AVSRFASTDPMLSPHIGAMVGOAAGHAIQYNTPLGKPDITLWWAGATLGAADLNKAEFEV 360
Qy      361  ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVQGRHPNPEDVVIDIESNG 420
      |||
Db      361  ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVQGRHPNPEDVVIDIESNG 420
Qy      421  LPHHNPSNHVDIFDIIQETRV 441
      |||
Db      421  LPHHNPSNHVDIFDIIQETRV 441
<!--EndFragment-->

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